Research 32:D138-D141, 2004). The protein HMM models were searched with program HMMPAM (Durbin et al., Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids, Cambridge University Press, 1998), with the default stringencies. A further filtering was done to keep only those matches with an expectation value of 0.1 or smaller as significant matches. Of the 20303 Corn rootworm peptide sequences, 4199 (21%) were identified with 1317 distinct protein domains and families.

[0373] The analysis results were presented in the feature fields of the sequence listing file with these attributes: Pfam name, Pfam description, and match level with HMMPFAM score, expectation value (E-value) and number of copies of the domain in the peptide sequence.

Example 16

[0374] This example illustrates a method for providing a DNA sequence for dsRNA-mediated gene silencing. More specifically, this example describes selection of an improved DNA useful in dsRNA-mediated gene silencing by (a) selecting from a target gene an initial DNA sequence including more than 21 contiguous nucleotides; (b) identifying at least one shorter DNA sequence derived from regions of the initial DNA sequence consisting of regions predicted to not generate undesirable polypeptides; and (c) selecting a DNA sequence for dsRNA-mediated gene silencing that includes the at least one shorter DNA sequence. Undesirable polypeptides include, but are not limited to, polypeptides homologous to allergenic polypeptides and polypeptides homologous to known polypeptide toxins.

[0375] WCR V-ATPase has been demonstrated to function in corn rootworm feeding assays to test dsRNA mediated silencing as a means of controlling larval growth. A cDNA sequence from a vacuolar ATPase gene (V-ATPase) from Western corn rootworm (WCR) (*Diabrotica virgifera* virgifera LeConte) was selected for use as an initial DNA sequence (SEQ ID NO. 40707). This initial DNA sequence was screened for regions within which every contiguous fragment including at least 21 nucleotides matched fewer than 21 out of 21 contiguous nucleotides of known vertebrate sequences. Three sequence segments greater than about 100 contiguous nucleotides that were free of such 21/21 hits were identified; a first sequence segment corresponding to nucleotide position 739-839, a second sequence segment corresponding to nucleotide position 849-987, and a third sequence segment corresponding to nucleotide position 998-1166 as set forth in SEQ ID NO:40707. These three sequence segments were combined to construct a chimeric DNA sequence (SEQ ID NO: 40772) for use in dsRNA-mediated gene silencing of the corresponding CRW V-ATPase coding sequence. The novel chimeric DNA sequence was tested in the CRW bioassay described above.

[0376] All publications, patents and published patent applications mentioned in this specification are herein incorporated by reference as if each individual publication or patent was specially and individually stated to be incorporated by reference.

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20120164205A1). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

1-45. (canceled)

46. A pesticide composition comprising a double-stranded RNA (dsRNA) that functions upon ingestion by a plant pest to inhibit the expression of a target sequence within said pest, wherein said composition is topically applied to a plant and provided in the diet of said pest.

47. The composition of claim **46**, wherein said dsRNA is comprised in a microbe that produces said dsRNA and is applied to the plant.

48. The composition of claim **47**, wherein said composition is topically applied using a spray mixer, is applied to the plant surface as matrix encapsulated RNA, or is applied as a seed coating.

49. The composition of claim **46**, wherein said plant pest is a Coleopteran pest selected from the group consisting of a *Diabrotica* spp. pest, a *Leptinotarsa* spp. pest, a *Tribolium* spp. pest, a *Anthonomous* spp. pest, a *Cyclocephala* spp. pest, and a *Polyphaga* spp. pest.

50. The composition of claim **49**, wherein said *Diabrotica* spp. pest is a corn rootworm pest selected from the group consisting of *Diabrotica virgifera* (Western Corn Rootworm, WCR), *Diabrotica barberi* (Northern Corn Rootworm, NCR), *Diabrotica virgifera* zeae (Mexican Corn Rootworm, MCR), *Diabrotica balteata* (Brazilian Corn Rootworm (BZR), *Diabrotica viridula* (Brazilian Corn Rootworm (BZR), *Diabrotica speciosi* (Brazilian Corn Rootworm (BZR)), and *Diabrotica undecimpunctata howardii* (Southern Corn Rootworm, SCR).

51. The composition of claim **46**, wherein said composition is topically applied as a seed coating.

52. A method for controlling pest infestation on a plant, comprising topically applying to said plant a pesticide composition comprising a dsRNA targeting for suppression of an essential gene in said pest and providing said plant in the diet of said pest.

53. The method of claim **52**, wherein said dsRNA is topically applied using a spray mixer, by expressing said dsRNA in a microbe and applying the microbe onto said plant, or by applying said dsRNA in a topical application further comprising at least a first *Bacillus thuringiensis* insecticidal protein.